

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: July 19, 2004, 17:15:05 ; Search time 17 Seconds  
(without alignments)  
3632.039 Million cell updates/sec

Title: US-09-920-953-2  
Perfect score: 1067  
Sequence: 1 ggcgtcgctgcagacgcggc.....agccattttcgaccacgccc 598

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US0920953/runat\_19072004\_171745\_23005/app\_query.fasta\_1.775  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPECL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US0920953 @CGN 1.1.27 runat\_19072004\_171745\_23005 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

- Database :
- 1: Issued Patents AA.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	136	12.1	345	4	US-09-920-953-2
C 2	134.5	12.0	170	4	US-09-920-953-2
C 3	134	11.9	663	4	US-09-920-953-2
C 4	130.5	11.6	308	4	US-09-920-953-2
C 5	129	12.1	1476	4	US-09-920-953-2
C 6	126	11.2	235	4	US-09-920-953-2
C 7	125.5	11.8	394	4	US-09-920-953-2
C 8	124	11.6	312	4	US-09-920-953-2
C 9	122	11.4	726	4	US-09-920-953-2
C 10	121.5	11.4	204	4	US-09-920-953-2
C 11	121.5	11.4	351	4	US-09-920-953-2
C 12	121	11.3	248	4	US-09-920-953-2

ALIGNMENTS

RESULT 1

US-09-252-991A-32377  
; Sequence 32377, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 32377  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32377

Alignment Scores:			
Pred. No.:	5,366-06	Length:	345
Score:	136.00	Matches:	70
Percent Similarity:	34.78%	Conservative:	10
Best Local Similarity:	30.43%	Mismatches:	64
Query Match:	12.12%	Indels:	86
DB:	4	Gaps:	10

US-09-920-953-2 (1-598) x US-09-252-991A-32377 (1-345)

QY 539 CAGGCTCTGGGCGCCCTGGGCGGCTGGCACTGGCGCTCCG---GCTCAAAATCGA 483

DB 101 GlnGlyProGlyGlyProGlyArgAspArgGlnValArgLeuProAlaAlaProGlyArg 120

Sequence 20509, A  
Sequence 23215, A  
Sequence 24725, A  
Sequence 32478, A  
Sequence 32006, A  
Sequence 26487, A  
Sequence 26899, A  
Sequence 20771, A  
Sequence 20122, A  
Sequence 30433, A  
Sequence 20543, A  
Sequence 21783, A  
Sequence 25365, A  
Sequence 18751, A  
Sequence 23674, A  
Sequence 16655, A  
Sequence 30765, A  
Sequence 29217, A  
Sequence 20790, A  
Sequence 20172, A  
Sequence 19128, A  
Sequence 24837, A  
Sequence 25813, A  
Sequence 29614, A  
Sequence 32359, A  
Sequence 24828, A  
Sequence 16788, A  
Sequence 24634, A  
Sequence 34470, A  
Sequence 28232, A  
Sequence 24009, A  
Sequence 31760, A  
Sequence 30043, A

QY 482 TGAATGAGCGCTCAGGCTGGGTTGGTTAATGAAATCAGTTGGGTGGCGAGTTGTTG 423  
 Db 121 ProSerArgGln-----SerArgLeu 128  
 QY 422 GNAAGTCAAAATCTCCGGGTGACTCCACCTCCGGGGCGGTGCTGGA----- 371  
 Db 129 GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgProSerProAla 148  
 QY 370 -----TCACATCC 363  
 Db 148 aTrpArgGlnProProlleGluLeuGlyAlaValArgLeuArgProProGlnArgArgP 168  
 QY 362 TGTTCAGCCCATCTCTTCAGCGCTCTCTCCAAAGTACTGCTTGTGATCTTGTCAAAATGG 303  
 Db 168 oAlaGlnArgProAlaValAlaAla----- 176  
 QY 302 CGTCTGCT-----CCAGGCGGTGGCCCTTGACCAGATGGGCGGTGCTGCTGATCATG 252  
 Db 177 -GlyGlyGlnArgGlnProGlyArgAspProAlaGluHisLeuArgProArgArgPro-- 195  
 QY 251 CTTCCGCCCTTGTATTGCTCTGCTCCGCCAACACACGAAAGCTCATCAACTTGACCTGCTTC 192  
 Db 196 -----GlyLeuLeuArgArgProArg-----ProAlaG 206  
 QY 191 ATCTCTGCTCTTGATCT-----CCAGGACTCGAAGAAG 156  
 Db 206 nProGlyArgLeuAlaSerGlyArgGlyAlaGlyGlyAlaGluProGlySerArgArg 226  
 QY 155 G-----GCAGCAGC 147  
 Db 226 sGlnValProGlyArgArgArgArgPropheArgSerProAlaGlyAlaaspArgAlaVa 246  
 QY 146 TCCGGGTGAGCAGCACCTTATCGTAGAAGTGTCAACCGCCAGCTTCATGCTTCTGCG 87  
 Db 246 lProGlyGluProArgProGlyProArgArgArgArgProGluArgProArgArgHi 266  
 QY 86 CGCCCCAGGTCTAT---CAACAGCTCTTGGCGCGCATCCGCTTCGCGCTCTCTG 30  
 Db 266 aArgProAlaHisGlyProGlyAlaGly-TyrProAlaAlaProLeuArgArgAlaGlyG 286  
 QY 29 GTGCTGGTGGCGGCTCTGCGAGCAG 4  
 Db 286 lYalaThrArgHisArgLeuArgGln 294

## RESULT 2

US-09-252-991A-19980  
 ; Sequence 19980, Application US/09252991A  
 ; Patent No. 6551795

## GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 19980

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19980

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
5,99e-06	134.50	170	68
Percent Similarity:	38.31%	Conservative:	9
Best Local Similarity:	33.83%	Mismatches:	45
Query Match:	11.99%	Indels:	79
DB:	4	Gaps:	15

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)  
 QY 524 CTTGGCGGCTCGGCAACTGGCGTCCCGCTCAA-----AATCATGGAATGAGCGC 471  
 Db 14 ProGlyArgArgAsnArgArgAlaAlaProAlaAlaAlaGlyArgArgSerAlaArg 33  
 QY 470 TCAGGCTGG-----GGTTGGGTTAATGAAATCAGTTGGGTGGCGAGTTGTTGGGAAG 417  
 Db 34 SerGlyTrpProCysGlyTrp-----Arg-TrpSerHisProCysTrp----- 47  
 QY 416 TCAATTCCTCCGGGTGAGCTCCACCACTCCGGGGCGGTGCTGATCAGATCAGATCTGCTTG 357  
 Db 48 -GlnHisArgArgArgProArgProSerArg-----SerArgProAlaAla 64  
 QY 356 AGCCCATCTCTTCAGCGCTCTCTCAAGTACTCTTGTCAAGTGGCGGTGG 297  
 Db 64 aArgPro-----SerGlyGlyAl 70  
 QY 296 TCCAGCGCTGGCCCTTGACAGAT-----GGCGGTGCTGCTGATGCTTCTCGG 246  
 Db 70 aAlaileArgArgProValProAspGlyGlnProGlyArgArgArgAsnAlaCys----- 88  
 QY 245 CCCTTGTATTGCTGCTCCGCCAACACAGAGCTCATGAAGTTCGCTTCTCATCTTC 186  
 Db 89 -----SerThrArg----- 91  
 QY 185 TGCTCTTCATGCTCCAGGACTCGA-----AGAAGGCGAGCAGC 147  
 Db 92 -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAl 108  
 QY 146 TCCGGGTGAG-----CCAGCACCTTATGCTAGA-----AG 117  
 Db 108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgArgSerAr 128  
 QY 116 GTGTCAACCGCCAGCTTCATGCTTCTGCGCGCCAGGTCATCAACAGGCTTCTTGGCG 57  
 Db 128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysSe 144  
 QY 56 CCGCATCCCGTTCGCG-----CGTCTCTGT-----GGTCTGCTGGCGCGCTCTGC 10  
 Db 144 r-AlaSerArgAsnArgSerArgSerCysSerArgSerGlySerAlaGlyArgSerCys 163

## RESULT 3

US-09-252-991A-30843

; Sequence 30843, Application US/09252991A

; Patent No. 6551795

## GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30843

; LENGTH: 663

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30843

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1,12e-05	134.00	663	53
Percent Similarity:	35.71%	Conservative:	17
Best Local Similarity:	27.04%	Mismatches:	71
Query Match:	11.94%	Indels:	55
DB:	4	Gaps:	13

RES001-3  
US-09-252-991A-29427  
Sequence 29427, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND  
TITLE OF INVENTION: AERUGINOSA FOR DIA  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,196  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 29427  
LENGTH: 1476  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29427

Alignment Scores:  
 Pred. No.: 5, 15e-05 Length: 1476  
 Score: 129.00 Matches: 74  
 Percent Similarity: 38.01% Conservative: 10  
 Best Local Similarity: 33.48% Mismatches: 91  
 Query Match: 12.09% Indels: 46  
 DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

QY 9 TCAGAGCGGCGCCACAGCAGCAGCAGCGCGGAGC-----GGATCGGG 56  
 Db 492 CysArgAlaHisArgGlnHisArgGlnAlaAlaAspAlaLeuGlyGlnArg 511  
 QY 57 GCGCAAGAGCTGTTGATGACTGGCGGCGCAGAGGCATGAAGCTGGCGGTGACAC 116  
 Db 512 ThrGlnLeuSerArg--ArgProGlyGlnLeuArgAlaProGlyHisArgAlaHis 530  
 QY 117 CTTCTACGATAAGTGTGCTGACCCGAGCTGCTGCTTCTTCAGTCCCTGGACAT 176  
 Db 531 LeuProGlnLeuGlyAlaAla---ValGlyGlyAlaGlyLeuArgArg-----GlyHis 547  
 QY 177 GCAAGAGCAGAAGATGAAGAGGTCAGTTCATGAGCTTCGTGTTGCGGAGCAGACCA 236  
 Db 548 ArgProGlyArgTrpProValGlyLeuValArg-----ArgArgLeuPro 562  
 QY 237 ATA-----CAAGGCGCGAAGCATGTACAGCCACAGCCCATCTGTTCAAGGCCACGG 290  
 Db 563 AlaGlyArgGlyThrArgArgGlnGlyArgThrArgArgProGlyProAla 582  
 QY 291 CTGGA-----CCACGGCA-----CTTGACAGATCAAGCAGTA 326  
 Db 583 ProGlyAlaGlyAlaAspArgProProAlaPheLeuLeuSerGlyAlaAlaArg 602  
 QY 327 CTTTGAGAGAGCGCTGCAAGAGATGGCGTCAA-----GCAGGATGTGATCCAGCAGC 380  
 Db 603 Pro--ArgArgAlaGlyProAspArgGlnProProAlaGlyProAspProGlyArg 621  
 QY 381 CCGCGAGTGTGAGTCCACCGC-----GACGAATTGACTNCCCAACAA 428  
 Db 622 ArgHisArgGlyAlaVal--ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr 641  
 QY 429 CTGCGACCAACTCATTTTCAATTAACCAACCCACAG----- 465  
 Db 641 OProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi 661  
 QY 466 ----CTGAGCGCTCATTCATCGATTTTGACGGGAGCGCCAGTTCGCGAGCGCGCC 521  
 Db 661 sProProGlyArgAspAlaArg-----AlaThrValArgProArgPr 676  
 QY 522 AGGGGCGCAGAGCGCTGCAATCTGTTGCCAGCCCTGCTGCTTGAAGAGCCATCAG 580  
 Db 676 OSerArgProAlaGly--GlnTyHisProProAlaArgValAlaGlyLysArgHisArg 695

RESULT 6

US-09-252-991A-24046  
 ; Sequence 24046, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 24046

; LENGTH: 235

; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-24046

Alignment Scores:  
 Pred. No.: 5, 38e-05 Length: 235  
 Score: 126.00 Matches: 47  
 Percent Similarity: 39.16% Conservative: 18  
 Best Local Similarity: 28.31% Mismatches: 58  
 Query Match: 11.23% Indels: 43  
 DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)

QY 482 TGAATGACGCTCAGGC---TGC-----GGTTGGTTAATGAAATCAG 441  
 Db 26 TrpAspGlyArgSerGlyArgTrpSerArgArgTrpCysAlaTrp----- 40  
 QY 440 TTGGGTGCGCAGCTGTGGGNAAGTCAAATTCGTGCGGTGGACTCCACACATCCGGCG 381  
 Db 41 ---GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59  
 QY 380 GCGTGTGATCAGATCCTCTGTCAGCCCATCTCTTCAGCGCTCTCCAGAGTACTGC 321  
 Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer----- 77  
 QY 320 TTGATCTTCAAGTGGCGGTGCTCCAGCGCTGACCCCTTGACACAGATGGCGGTGCG 261  
 Db 78 -----ArgArgTrpThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91  
 QY 260 TGTACATGCTTCGGCCCTTGATTGCTGCTCGCCCAACACACAGCTCATGAACCTG 201  
 Db 92 -----ThrProProPro-Thr----- 96  
 QY 200 ACTGCTTCTATCTTCTGCTTTCATGCTCCAGGACTGAAGAGGCGAGCAGCTCCGG 141  
 Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerLysHisAlaAlaProG 114  
 QY 140 TCAGCCAGCACCTTATCGTAGAAGGTGT-----CAACCGCCAGCTTCATGCT 93  
 Db 114 yValSerAlaSerAlaSerAlaArgCysAlaCysCysSerSerProGlySerGlyG 134  
 QY 92 TGTGCGCCCGCAGGTATCAACAGCTTCTTTCGCGCCGATCCCGCTTCGCGCTCTCT 33  
 Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153  
 QY 32 GTGGTCTGCTGGCGCG 17  
 Db 153 gtrpProArgtrpPro 158

RESULT 7

US-09-252-991A-19344  
 ; Sequence 19344, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 19344  
 ; LENGTH: 394  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-19344



FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20675  
LENGTH: 726  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20675

Alignment Scores:  
Pred. No.: 0.000219 Length: 726  
Score: 122.00 Matches: 74  
Percent Similarity: 32.13% Conservativeness: 5  
Best Local Similarity: 29.72% Mismatches: 74  
Query Match: 11.43% Indels: 95  
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)

```
QY 2 CGCTCCCTGCAGAG-----CGGCCACACACACAGAGCGCGGAGCGGATGCG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAlaAr 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 GCGCAAGAAGCTGTTTCATGACCTTGGCGCGCGAGAGG-----CATGAAGC 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 g-----ProAlaAlaArgArgAlaAlaValGlyGluAl 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 104 TGGC-----GGTTGACACCTTCTACGATAAGTGTCTGGC-----TGACCGGAGC 148
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 aglyAlaAlaGlyGlnGlyProArgThrGlyAlaAlaArgThrGlnInserProGly: 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 149 TGCTCCCTTCTTCAGTCCCTGGACATGCAAGAGCAGAGCAGAGTGAAGTCAAGTTCA 208
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGlySerAla-----AlaGl 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 209 TGAGCTTCGTGT-----TGG----- 224
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 -----CGGAGCAGACCAATACAGG 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 oAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 GCGAAGCATGTACGACGACACACGCCCATCTGTTCAAGGGCCCGCTGGACACCGCC 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProPr 429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 ACTTTGACAA-----GATCAA-----GCAGTACTTGGAGAGCGCTGCAAG 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaAlaProGlyArgAspAlaAlaAr 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 347 AGAT----- 350
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 351 -----GGCGTCAAGCAGGATGTATCCACACCGCGCGGAGTGTGAGT 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyAl 489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 CCACCGCGACGAATTTGACTTCCCAACACTGGCCACCACTGATTTTCATTAAACC 457
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 AACCCCGAGCTGAGCGCTCATTCATTCGATTTTGTAGCGGAGCGCCAGTTGCCAGCGC 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 o-----HisGlyArgArgHisLeuProProAl 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 GCCCAGGGGGCCAGGAGCGCTGCAA 542
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 512 aGlnArgGlyGluProAlaLeuArg 520

## RESULT 10

US-09-252-991A-17837  
Sequence 17837, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 17837  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17837

Alignment Scores:  
Pred. No.: 0.000154 Length: 204  
Score: 121.50 Matches: 60  
Percent Similarity: 34.56% Conservativeness: 15  
Best Local Similarity: 27.65% Mismatches: 77  
Query Match: 11.39% Indels: 65  
DB: 4 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

```
QY 5 TGCTTSCAGACGGCGCCACACACACAGAGACGGCGGAGCGGATGCGGGGCCAAGA 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 CysSerSerThrArgProThrProThrTrp-----ProSerAlaAsn 21
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 ACCTGTTTCATGCTGGCGCGGAGGAGGATCAAGCTGGCGGTTCACACCTTCTACG 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 SerMetAlaThrAlaTrpProPheProAlaAlaSerTrpArgArgThr-----Thr 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 125 ATAAGTGTCTGG-----CTGACCGCGAGCTGC----- 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 SerArgCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 TGCCCTTCTTCAGTCCCTGGACATGCAAGACAGACAGATGAAGCAGGTCAAGTTTCATGA 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProProArgSerSer----- 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 GCTTCGTGTTGGCGGAGCAGCAATACAGGGCGGAGCATGTACGACGACACGCC 271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 -----ArgGluProGluProCys-----ArgAlaPro 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 ATCTGTCAAGGGCCACGCCCTGGACCCACCACCTTTGACAGATCAAGCAGTACCTTG 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ProTrpSer-----AlaAlaTrp-----AlaAlaThrCys 95
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 GAGAGACGCTGCAAGAGATGGCGGTCAAGCAGGATGTATCCAGCACGCGCGGAGTGG 391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 392 TGGAGTCCACCGCGCAGAAATTTGACTTNNCCCAACACTGCGCACCCCACTGATTTTCAT 451
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 ThrLeuProThrProGlySerAlaAlaProAlaCysAlaSerGlyIle----- 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 452 TAACCCCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGTAGCGGGGAGCGCGCAGTT--- 508
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProPro 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 509 -----GCCGAGCGCGCCAGGGGGGCCAGAGCGCTCAATCGT 547
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 144 ArgSerProArgArgGlyTyrSerGluSerMetArgTyrCysTyrGlnProAla----- 161  
QY 548 TTGCAGCCCTTGTGCTGATTAAGAGCATCAGCATTTTCGACCAAGCC 598  
Db 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgArgAla 177  
RESULT 11  
US-09-252-991A-18476  
; Sequence 18476, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18476  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18476  
Alignment Scores:  
Pred. No.: 0.000188 Length: 351  
Score: 121.50 Matches: 58  
Percent Similarity: 33.50% Conservative: 10  
Best Local Similarity: 28.57% Mismatches: 58  
Query Match: 11.39% Indels: 77  
Gaps: 4  
DB: 10  
US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)  
QY 30 CACAGACGCGGAGCGGATCGCGGCGCAGACCTGTTGATGACCTGGCGCGCC 89  
Db 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArg 150  
QY 90 AGA-----AGCATGAAGCTGGCGGTGACACCTTCTACGATAAGGT 131  
Db 151 LysProAlaValArgProAlaAlaArgHisAlaAlaProAla----- 163  
QY 132 GCTGGCTGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGGA-----CATGCA 179  
Db 164 -----ProGlyLysAspProArgArgArgArgGlyAspGlnGluProHisArg 180  
QY 180 AGACGAGAAGATGAAGCAGCTCAAGTTCATGAGCTTGTGTTGGCGGACCAATA 239  
Db 181 AlaAlaArgArgAlaGlyGlyAlaHis-----ArgProTyrArg-----ArgProLeu 197  
QY 240 CAAGGCGCGAAGCATGTACGACGACACGCGCCATCTGGTCAAGGCGCACCGCTGGACCA 299  
Db 198 ProGlyProAspHisProArgGlyGlyGlnProAlaGlyGlyLeuProHisAla----- 215  
QY 300 CCGCCACTTTGACAGATCAAGCATCAAGTACCTTGGAGAGACCTGCAAGAGATGGCGTCAA 359  
Db 216 -----AlaIleArgArgGlyArgGln 222  
QY 360 -----GCAGATGTGATCCAGCA-----CGCCGCGCG 386  
Db 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg 242  
QY 387 AGTGGTGGATTCACCGCAGCAAGATTGATTNCCCAACAACCTGCGCACCCCACTGATT 446  
Db 243 ProGlyAlaValAlaProAlaAlaArgLeuGlyAsnLeuAlaGlyGlnAlaGln----- 260  
QY 447 TTCATTAAACCAACCCAGCGCTGACGCTCATTCCTCGATTGAGCGGGAGCGCCAG 506  
Db 261 -----GlyArgArgAla 264

QY 507 TTGCCG-----AGCGCCCGCAGGGGGCCCGAGGAGC 536  
Db 265 GlyProArgArgArgArgAlaAlaArgHisLeuArgProProArgArgProArgArg 284  
QY 537 CTGCAATC 545  
Db 285 LeuArgVal 287  
RESULT 12  
US-09-252-991A-20161  
; Sequence 20161, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20161  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20161  
Alignment Scores:  
Pred. No.: 0.000187 Length: 248  
Score: 121.00 Matches: 47  
Percent Similarity: 35.11% Conservative: 19  
Best Local Similarity: 25.00% Mismatches: 62  
Query Match: 11.34% Indels: 60  
Gaps: 4  
DB: 11  
US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)  
QY 2 CGCTCGCTGCAGACGCGGCGCACACCA-----CACAGACGCGCGGAGCGGATCGGGC 58  
Db 56 ArgCysAlaArgSerProProAlaGlyProSerSerThrThrArgArgProAlaSer 75  
QY 59 GCAAGA---AGCTGTTGATGACCTGGCGGCGGAGAGGATGAAGTGGCGGTGACA 115  
Db 76 AlaSerIleArgCys-----SerAlaArgValArgLysTyrTrpSerThr 90  
QY 116 CTTTCTACGATAAG----- 130  
Db 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgArgTrpCysArg 110  
QY 131 -----TGTGGCTGACCGGAGC-----TGCTGC----- 154  
Db 111 ArgCysAlaCysTyr---ThrArgAsnArgProAlaArgSerCysArgCysValAla 129  
QY 155 -----CCTTCTCGAGTCCCTGGACATGC 178  
Db 130 ThrArgSerSerAlaProProThrThrProAlaProThrSerIleProThrProCys 149  
QY 179 AAGACGAGAAGATGAAGCAGGTCAAGTTCATGAGCTTGTGGCGGAGCAGACCAAT 238  
Db 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla----- 159  
QY 239 ACAAGGCGCGAAGCATGTACGACGACACGCGCCATCTCGTCAAGGCGCACCGCTGGACC 298  
Db 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTyrArgSerAlaGlySerThrAla 178  
QY 299 ACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGAGACCTGCAAGAGATGGCGTCA 358  
Db 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196

```

US-09-252-991A-23215
; Sequence 23215, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23215
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23215

Alignment Scores:
Pred. No.: 0.000228 Length: 219
Score: 120.00 Matches: 57
Percent Similarity: 38.27% Conservative: 18
Best Local Similarity: 29.08% Mismatches: 72
Query Match: 10.70% Indels: 49
DB: Gaps: 9

```

[illegible]



```
; Sequence 24725, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24725
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24725

Alignment Scores:
Pred. No.: 0.000253 Length: 209
Score: 119.50 Matches: 55
Percent Similarity: 33.04% Conservative: 19
Best Local Similarity: 24.55% Mismatches: 73
Query Match: 10.65% Indels: 77
DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-24725 (1-209)
QY 497 CCGGCTCAAAATCGATGAATGAGCGCTCAGGCTGG-----GGTTGG 456
DB 5 ProThrArgArgSerAlaAlaArgSerTrpSerAlaAlaArgSerAlaGlyTrp 24
QY 455 GTTAAATGAATCATGTTGGTGGCAGTTG-----TTGGNAAGTCMAATTCGTG 405
DB 25 LysP-oArgThrIleProGlySerArgSerAlaThrGlyTyrSerArgProThrAlaGly 44
QY 404 CGGTGGGACTCCACACTCCGGCGCGTGGATCACATCCTGTTG----- 357
DB 45 ArgThrThrArgPheProThrAlaAlaAlaTrpArgAlaTrpAlaSerArgSerIle 64
QY 356 -----ACGCCATCTTGTGAGCGTCTCTCCAAAGTACTGCTTGTATCTTGTCAAAGTGG 303
DB 65 ArgProThrProTrpAlaCysSerAlaCysProAla----- 76
QY 302 CGGTGGTCCAGCGCTGCGCCCTTGACACAGATGGCGGTGCTGCTACATG----- 252
DB 77 -----SerProPro-----ThrTrpAlaCysSerThrSerAlaSerProArg 90
QY 251 ---CTTCGCGCCTTGTATTGTCTGCTCCGCCAAACACGAAGCTCATGACTTGACCT-- 197
DB 91 ProAlaArgProTrpTrpProProProGly-ArgSerAla-----ProPr 107
QY 196 -----GTTTCATCTTCTGCTCTT-----GCATGTCAGGGACTCGAAG 159
DB 107 oSerAspArgSerAlaSerArgAlaAlaGluTrpSerAlaSerProAlaValArgLy 127
QY 158 AAGGCACGACGTCGGGTGTCAG----- 137
DB 127 sasnAlaAlaThrProCysArgCysSerAlaSerMetProAlaSerThrThrMetProAr 147
QY 136 -----CCAGCACCTTATCGT----- 122
DB 147 gThrSerProAsnAspTrpProArgProAlaArgThrAlaSerThrSerIleThrArgth 167
QY 121 -----AGAGGTCTCAACCGCAGCTTCATGCTTCTGCGCGCCCGGCTCATCA 72
DB 167 rSerAlaAlaArgSerThrProSerArgCysSerThrProArgProGlySerAr 187
QY 71 AACAGCTTCTTGGCCCGCATCCCGCTTCCCGCGCTCTCTGTGTGCTGTGCGCGCTCT 12
DB 187 gSerAlaAlaSerProThrThrThrThrProSer-CysHisProGlyArgThrAlaC 207
```

```
QY 11 GCAGGCAG 4
DB 207 ysArgArg 209
```

```
Search completed: July 19, 2004, 17:20:42
Job time : 24 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: July 19, 2004, 17:19:11 ; Search time 46 Seconds  
(without alignments)  
8126.576 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1067

Sequence: 1 gcgcctgcgcacgcggc.....agccatttcgcaccagcc 598

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delgap 6.0 , Delext 7.0

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 2570690

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp  
-Q=/cgn2\_1/USPO\_specol\_P/US09920953/runat\_19072004\_171746\_23038/app\_query.fasta\_1.775  
-DB=Published Applications AA -QPMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIAGONAL2  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -WAP=US09920953 @Cgn1 1 13 @runat 19072004 171746 23038  
-NCPU=6 -ICPU=3 -NO MMAR -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/pct\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
-----				

RESULT 1

US-10-282-122A-61519  
; Sequence 61519, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848

ALIGNMENTS

Sequence 61519, A  
Sequence 58160, A  
Sequence 5, Appli  
Sequence 143835,  
Sequence 3, Appli  
Sequence 6, Appli  
Sequence 8, Appli  
Sequence 166380,  
Sequence 72136, A  
Sequence 72137, A  
Sequence 5, Appli  
Sequence 7, Appli  
Sequence 103601,  
Sequence 141171,  
Sequence 63797, A  
Sequence 63798, A  
Sequence 63800, A  
Sequence 63691, A  
Sequence 47573, A  
Sequence 40384, A  
Sequence 46621, A  
Sequence 48205, A  
Sequence 4, Appli  
Sequence 176482,  
Sequence 106950,  
Sequence 65735, A  
Sequence 6510, A  
Sequence 6, Appli  
Sequence 168168,  
Sequence 64278, A  
Sequence 5426, A  
Sequence 3, Appli  
Sequence 67798, A  
Sequence 61224, A  
Sequence 53493, A  
Sequence 128400,  
Sequence 132079,  
Sequence 4, Appli  
Sequence 56601, A  
Sequence 70729, A  
Sequence 104973, A  
Sequence 38596, A  
Sequence 8, Appli  
Sequence 50473, A  
Sequence 126060,

; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 61519  
 ; LENGTH: 124  
 ; TYPE: PRT  
 ; ORGANISM: Legionella pneumophila  
 ; US-10-282-122A-61519

Alignment Scores:  
 Pred. No.: 1,49e-15 Length: 124  
 Score: 254.50 Matches: 49  
 Percent Similarity: 64.10% Conservative: 26  
 Best Local Similarity: 41.88% Mismatches: 41  
 Query Match: 23.85% Indels: 1  
 DB: 12 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)

QY 61 AAGAGCTGTTGATGACCTGGCGCGGCGAGGATGAGCTGGGGTTGACACCTTC 120  
 Db 3 GluSerLeuPheGluArgLeuGlyGlnAenAlaValAsnThrAlaValAspIlePhe 22  
 QY 121 TACGATAAGTCTCGCTGACCGGAGCTGCTGCGCTTCTCGAGTCCCTGGACATGCAA 180  
 Db 23 TyrArgLysMetLeuMetAspArgValAsnTyrPhePheAspValAspMetGlu 42  
 QY 181 GAGCAGAGATGAAGCAGTCAAGTTTCATGAGCTTCGTTGTCGCGAGCAGACCAATAC 240  
 Db 43 GlnGlnIleLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62  
 QY 241 AAGGCGGAAGATGATGACGACACACCCATCTGTCAGGCGGCGGCTGGACCAAC 300  
 Db 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81  
 QY 301 CCCCACTTTGACAGATCAAGCAGTACCTTGAGAGACGCTGCAAGAGATGGCGTCAAG 360  
 Db 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101  
 QY 361 CAGGATGTGATCCACACCGCGGAGTGTGGAGTCCACCCCGGACGAA 411  
 Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2

US-10-425-114-58160  
 ; Sequence 58160, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 58160  
 ; LENGTH: 324  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07\_FLI pep  
 ; US-10-425-114-58160

Alignment Scores:  
 Pred. No.: 2.9e-05 Length: 324  
 Score: 148.00 Matches: 62  
 Percent Similarity: 38.10% Conservative: 18  
 Best Local Similarity: 29.52% Mismatches: 77  
 Query Match: 13.87% Indels: 53  
 DB: 12 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)

QY 5 TGCTCCAGACGGG-----CCACCAGACACACAGACGGCGGAGCGG 49  
 Db 84 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgArgThr 103  
 QY 50 GATCGGGCGGCAAGAGCTGTTGATGACCTGGCGGCGCAGAGGCATGAAGCTGGCGG 109  
 Db 104 SerSerGlySerArgAlaCys-----110  
 QY 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTACCCGAGCTGTGTC 154  
 Db 111 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 128  
 QY 155 CCTTCTTCGAGTCCCTGGACATGCAAGACGACAGATGAAGCAGGTCAAGTTCATGAGCT 214  
 Db 129 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerArgAla 147  
 QY 215 TGTGTTTCGGGAGCAGACCAATACAGGCGCGGAGCATGTACGACGACACGCGCATC 274  
 Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgArgProGln 167  
 QY 275 TGCT-----CAAGGCCACGCGCTGGACCCGACCTTTGACAGATCAAGCAGTACC 328  
 Db 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 186  
 QY 329 TTGAGAGACGCTGCAAGAGA-----TGGCGCTCAAGCAGGATGTGATCC 373  
 Db 187 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 204  
 QY 374 AGCACGCCCGGAGTGTGGAGTCCACCGCGGACGAATTCACCTNCCCACTCGG 433  
 Db 205 AlaCysAlaThrProThrTrpArgProAlaProArgCysThrAlaSerAlaThr--- 223  
 QY 434 CACCCAACTGATTTTCATTAAACCCACCCAGCGCTCATTCCTCATGATTTTTCAG 493  
 Db 224 -----ProGlnAlaAlaAlaSerGlyThrSerTrpArg 234  
 QY 494 -----CGGGAGCGGCGAGTTCGCGAGCGGCCAGCGGCGCCAGGAGGCTGCA 541  
 Db 235 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253  
 QY 542 AATCGTTTCCAGCCCTTCTGCA 565  
 Db 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3

US-10-084-846A-5  
 ; Sequence 5, Application US/10084846A  
 ; Publication No. US20040006026A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEITNAUER, GABRIELE  
 ; APPLICANT: MUHLENWEG, AGNES

/	APPLICANT:	TREFZER, AXEL
/	APPLICANT:	BECHTHOLD, ANDREAS
/	TITLE OF INVENTION:	AVILAMYCIN DERIVATIVES
/	FILE REFERENCE:	1974-005
/	CURRENT APPLICATION NUMBER:	US/10/084,846A
/	CURRENT FILING DATE:	2003-02-25
/	PRIOR APPLICATION NUMBER:	PCT/EP01/09815
/	PRIOR FILING DATE:	2001-08-24
/	PRIOR APPLICATION NUMBER:	DE 101 09 166.4
/	PRIOR FILING DATE:	2001-02-25
/	NUMBER OF SEQ ID NOS:	120
/	SOURCE:	Patentin Ver. 3.2
/	SEQ. ID NO. 5	
/	LENGTH:	19723
/	TYPE:	PRT
/	ORGANISM:	Streptomyces viridochromogenes
/	FEATURE:	
/	OTHER INFORMATION:	Protein 3: amino acid sequence encoded by coding strand 1.
/	OTHER INFORMATION:	Start codon: atc, Start position: nucleotide 3.
/	US-10-084-846A-5	
 Alignment Scores: Pred. No.: 0.000252 Length: 19723 Score: 142.50 Matches: 63 Percent Similarity: 34.96% Conservative: 16 Best Local Similarity: 27.88% Mismatches: 68 Query Match: 13.36% Indels: 79 DB: 15 Gaps: 12		
 US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)		
Qy	5	TGCGTGCAGACGGCCACCACGACACACGAGACGCCGGAAGCGGGATGGCGGCAAGA 64
Db	4635	CysAlaAlaArgSerProSerPro-----AlaTrpSerThr 4647
Qy	65	AGCTGTTCGATGACCTGG-----CGGGCGAGAAGCGCATGAGCTGCGGTG 112
Db	4648	SerAlaProAlaThrTrpSerTrpTrpSerAlaAlaThrAlaProCysTrpArgPro 4667
Qy	113	ACACCTTCACATAAGGTCGTGGCTG-----139
Db	4668	ThrProProThrGlyProAlaTrpSerGluTrpThrProProProSerSerProArg 4687
Qy	140	----ACCGG-----AGCTGTCGCCCTTTCTTCAGATCCCTGGACATGCAAGACGAGAAGA 190
Db	4688	ProThrArgArgAlaSerSerSerProThrSerHisThrTrpCysSerAlaGlyAla 4707
Qy	191	TGAAGCAGTCAAGTTCATGACTTCGTG-----TTGGCGGACGACACC 235
Db	4708	AlaProArgSerSerProArgSerArgCysSerThrTrpCysArgValProTrpSerSer 4727
Qy	236	AATACAAGGCCGAACATGTACGACG-----262
Db	4728	CysGlyArgSerAlaAlaCysargThrThrAlaSerGlyProSerArgAlaIleCysPro 4747
Qy	263	-----CACAGCCC-----ATCTGGTCAAGGGCCAGCGCTGGACCCGCCCACT 307
Db	4748	ArgCysSerThrProAlaProThrThrTrpSerAlaThrSerThrTrpThrThrThrGly 4767
Qy	308	TTGACAAGATCAAGCAGTAGTACCTTGAGAGACGCTGAAAGAGATGGCGCTCAAGCAGGATG 367
Db	4768	CysAlaArgSerSerGly-----TrpProSerAla-----4777
Qy	368	TGATCCAGCAGCGCCGCCGAGTGGTG-----AGTCACCGCGGAGCAATTACTTNC 421
Db	4778	-----ProAlaArgTrpMetProSerProSerThr--AlaGluAlas 4793
Qy	422	CCAACAACCTGCGCACCACTGATTTTCATTAAACCAA-----459
Db	4793	erArgSerCysTrpProAlaAlaAlaProLeuAlaArgSerThrSerArgTrpProA 4813
Qy	460	--CCCCAGCTGAGCGCTCATTCCTCCATCGATTTTGAGCGGGGAGCCCGAGTTCGCGAGCGC 517

**D**b   **4813 laSerAlaProGluArgArg-----ThrCysProThrArgSerS 4826**

**Q**y     **518 GCCACGGGGGCCCA 531  
                |||||**

**D**b       **4826 erProgIyGlyPro 4830  
                |||||**

**R E S U L T   4**

**U**S-**10-437-963-143835**  
**; Sequence 143835, Application US/10437963**  
**; Publication No. US20040123343A1**  
**: G E N E R A L I N F O R M A T I O N :**  
**; APPLICANT:** La Rosa, Thomas J.  
**; APPLICANT:** Kovalic, David K.  
**; APPLICANT:** Zhou, Yihua  
**; APPLICANT:** Cao, Yongwei  
**; APPLICANT:** Wu, Wei  
**; APPLICANT:** Boukharov, Andrey A.  
**; APPLICANT:** Barbazuk, Brad  
**; APPLICANT:** Li, Ping  
**: T I T L E OF INVENTION:** Rice Nucleic Acid Molecules and Other Molecules Associated With  
**: T I T L E OF INVENTION:** Plants and Uses Thereof for Plant Improvement  
**: FILE REFERENCE:** 38-21(53221)B  
**: CURRENT APPLICATION NUMBER:** US/10/437,963  
**: CURRENT FILING DATE:** 2003-05-14  
**: NUMBER OF SEQ ID NOS:** 204966  
**: SEC ID NO 143835**  
**: LENGTH:** 417  
**: TYPE:** PRT  
**: ORGANISM:** Oryza sativa  
**: FEATURE:**  
**: OTHER INFORMATION:** Clone ID: PAT\_MRT4530\_44705C.1.pep  
**U**S-**10-437-963-143835**

**A l i g n m e n t   S c o r e s :**

Pred.	No.:	Score:	Length:
		0.00488	417
		125.00	Matches:
		36.19%	Conservative:
		30.00%	Mismatches:
		11.72%	Gaps:
		16	Indels:
			10

**U**S-**09-920-953-2 (1-598)** x **U**S-**10-437-963-143835 (1-417)**

<b>Q</b> y	<b>23 CCAGCACACAGAGACCGGCAGAAGCGGATGGCGCGGAAGAGCTGTTTGACTGACCTGG 82</b>
<b>D</b> b	<b>                    :::    </b>
<b>Q</b> y	<b>22 ProThrPrOHISerArgArgglu-----flegluArgTrp 32</b>
<b>Q</b> y	<b>83 CGCGCGCAGAAGCATGAAGTGGGGTGACACCTTCACGATAAGGTCTGGTGCCTGACC 142</b>
<b>D</b> b	<b>                       </b>
<b>Q</b> y	<b>33 Leu-----ProTripgserAlaProPropro-----ThrThr 43</b>
<b>Q</b> y	<b>143 CGGAGCTGCTGC-----CCTTCTTCGATCCCTGGACATGCAGACGACA 187</b>
<b>D</b> b	<b>                             </b>
<b>Q</b> y	<b>44 GlySerCysSerThrProThrThrProProProProProProProProProProProSer--- 62</b>
<b>Q</b> y	<b>188 AGATCAAGCAGGTCAAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAATACAAGGGCC 247</b>
<b>D</b> b	<b>                             </b>
<b>Q</b> y	<b>63 -----SerArgsserLeuproProlathrProproProalaprothrlysarga-g--- 79</b>
<b>Q</b> y	<b>248 GAAGCATGTACGACGACACGCCCATCTGGTCAAGGGCCACGGCTGGACCCACCCTGCACT 307</b>
<b>D</b> b	<b>                                     </b>
<b>Q</b> y	<b>80 -----ArgThrThrArgTrp----GlyAlaThr 87</b>
<b>Q</b> y	<b>308 TTGACNAGATCAAGCAGTAGCTTGGAG-----AGACGCTGCAAG 346</b>
<b>D</b> b	<b>      Thr:                         </b>
<b>Q</b> y	<b>88 LeuthrAlaThrThrSerThralagluasnSerArgArgArgThrArgArgAlaArgArg 107</b>
<b>Q</b> y	<b>347 AGATGGGGCTCAAGCAGGATTGTATCCAGCAGCGCGCGAGTGTGGAGTCCA----- 400</b>
<b>D</b> b	<b>                                     </b>
<b>Q</b> y	<b>108 ArgArgGlyArgSerArgAlaSerSerThrThrProProProProProProProProglyThr 127</b>
<b>Q</b> y	<b>401 ---CCCggcagaatttgacttncccaacaacgctggccaccacctgatgttcatttaacc 457</b>
	<b>   </b>

Db 128 SerProSerThrProSerAlaAlaProSerThrSerSerProThrArgAlaSerProPro 147  
 QY 458 AACCCAGCTGAGCGCTCATTCATCGATTGTGAGCGGGAGCGCCAGTGGCCGAGCGC 517  
 Db 148 TyrArgSerThrSerProSerProPro--ProAlaAlaSerSerAlaSerAlaAla 167  
 QY 518 GCCAGGGGGCCCA-----GGAGCCTGCAAAATCGTTTG 550  
 Db 167 rProProAlaProThrThrSerProThrArgProProSerGlyCysAlaSerLeuA 187

QY 551 CGAGCCTTGCTGCATTGAAGGCCA 576  
 Db 187 laThrProAlaThrThrSerThrPro 195

## RESULT 5

US-10-084-846A-3  
 ; Sequence 3, Application US/10084846A  
 ; Publication No. US20040006026A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEITNAUER, GABRIELE  
 ; APPLICANT: MUHLENWEG, AGNES  
 ; APPLICANT: TREPZER, AXEL  
 ; APPLICANT: BECHTHOLD, ANDREAS  
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
 ; FILE REFERENCE: 1974-005  
 ; CURRENT APPLICATION NUMBER: US/10/084,846A  
 ; PRIOR FILING DATE: 2003-02-25  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4  
 ; PRIOR FILING DATE: 2001-02-25  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 3  
 ; LENGTH: 19695  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces viridochromogenes  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.  
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.  
 US-10-084-846A-3

Alignment Scores:  
 Pred. No.: 0.0119 Length: 19695  
 Score: 125.00 Matches: 57  
 Percent Similarity: 35.29% Conservative: 15  
 Best Local Similarity: 27.94% Mismatches: 68  
 Query Match: 11.72% Indels: 64  
 DB: 15 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)

QY 2 CGCTCCCTGCAAGC---CGGCCACACACACAGACGCGGAGCGGATCGCGGC 58  
 Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgSerArgSerProAla 11343  
 QY 59 GCAACA-----AGCTGTTTGATGACCTGGCGGCGCAGAGCGATGAGC 103  
 Db 11344 AlaArgThrTyrArgGlyAlaAlaSerThrThrProAlaAlaGlyArg----- 11361  
 QY 104 TGGCGGTTGACACCTTCTACGATAGG-----TCCTGG----- 1136  
 Db 11362 -----SerAlaValArgLysAsnCysTrpSerSerThrProArgPro 11376  
 QY 137 -----CTGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGACATGC 178  
 Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpPro 11396  
 QY 179 AAGACGAGAAGATGAAGCAGGTCAAGTTCA-----TGAGCTTCGTGTTG 223  
 Db 11397 AspSerProCysProArgCysSerSerTrpThrSerProProAlaSerThrArg 11416  
 QY 224 CGGAGCAGAC-----AATACAGGCGGAGGACGATGT 256

Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerSerArgAlaProProCys 11436  
 QY 257 AGAACACACACGCCCATCTGGTCAAGGGCCACGGCTGGACACCGCCACTTTGACAGA 316  
 Db 11437 CysSerProArgSerThrTrpArg-----ProThrGlySerProThrArg 11452  
 QY 317 TCAGACAGTACCTTGCAGAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376  
 Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466  
 QY 377 AGCCCGCCGAGTGTGGAGT-----CCACCCCGCAGC--- 409  
 Db 11467 ArgProSerProTrpTrpAlaAlaThrGlySerTrpProTrpArgProProArgThrCys 11486  
 QY 410 -----AATTGACTTCCCAACAACTGGCAGCAGTATTTTCAATTAACCCAAC 460  
 Db 11487 ArgProProArgLysSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506  
 QY 461 CCAGCCTGAGC 472  
 Db 11507 ProAlaValSer 11510

## RESULT 6

US-10-084-846A-6  
 ; Sequence 6, Application US/10084846A  
 ; Publication No. US20040006026A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEITNAUER, GABRIELE  
 ; APPLICANT: MUHLENWEG, AGNES  
 ; APPLICANT: TREPZER, AXEL  
 ; APPLICANT: BECHTHOLD, ANDREAS  
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
 ; FILE REFERENCE: 1974-005  
 ; CURRENT APPLICATION NUMBER: US/10/084,846A  
 ; PRIOR FILING DATE: 2003-02-25  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4  
 ; PRIOR FILING DATE: 2001-02-25  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 6  
 ; LENGTH: 19662  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces viridochromogenes  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.  
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.  
 US-10-084-846A-6

Alignment Scores:  
 Pred. No.: 0.0133 Length: 19662  
 Score: 124.50 Matches: 56  
 Percent Similarity: 33.02% Conservative: 14  
 Best Local Similarity: 26.42% Mismatches: 64  
 Query Match: 11.10% Indels: 78  
 DB: 15 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)

QY 536 GTCCTGGCCCGCTGGCGCGCTCGCAACTGGCG---CTCCCGCTCAAAATCGATGG 480  
 Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347  
 QY 479 AATGACGCTCAGCTGGGTTGGGTTAATGAATCAGTTGGGTGGCGCAGTTGTGGGN 420  
 Db 19348 -----ProGlyProGlyTrp----- 19352  
 QY 419 AAGTCAAAATTCGCGGGGTGGACTCCACCACTCGCGGGGCTGTGTGATCACAATCC--- 363  
 Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368

QY 362 -----TGCTTGACGCCCATCTCTTGCAGCGTCTCTCCA 330  
Db 19369 ArgCysSerGlyArgSerArgCysThrAlaCysSerCysProCysAlaSer 19388  
QY 329 AGGTACTGC-----TGCTTCTGTCAAGTGGCGG-----TGCTCAGG----- 291  
Db 19389 ArgArgCysGlyCysAlaGlyAlaThrTrpArgProArgTrpTrpTyrA-gSerPro 19408  
QY 290 ---CCGTGGCCCTTGACCATGGCGGTGCGTGTACATGCTTGGCCCTTGATGG 234  
Db 19409 SerProTrpGlyTrpCysArgTrpProThrAlaAlaGlyGlySerAlaAspThrTrpGly 19428  
QY 233 TCTGCTCGCCAAACACG----- 216  
Db 19429 SerSerProProSerProProArgProGlyGlyCysThrGluGlyArgSerProValSer 19448  
QY 215 -----AGCTCATCAACTTCACTGCTTCTCTCTCTTGCATGTCAGG 168  
Db 19449 SerProHisGlyArg-SerGlyCysTrpProAlaGlyProArgProAlaAlaGlyProGI 19468  
QY 167 GACTCGAAGAGGCGAGCAGCTCCGGGTGACCCAGCACCTTATCGTAGAAGGTGTCAACC 108  
Db 19468 YAspArgArgGlnAlaLeuSerSerGlySerPro----- 19479  
QY 107 GCCAGCTTCAGCTTCTGCGCCGCCAGGTGTCATCAACAGCTTCTTGGCCCGCATCCC 48  
Db 19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgIleAl 19493  
QY 47 GCTTCCG-----CCGTCTCTGTGTGCTGGTGG 20  
Db 19493 aAlaProThrIleProAlaLeuPheCysSerTrp 19504

RESULT 7

US-10-084-846A-8  
; Sequence 8, Application US/10084846A  
; Publication No. US2004006026A1  
; GENERAL INFORMATION:  
; APPLICANT: WEITNAUER, GABRIELE  
; APPLICANT: MUELENWEG, AGNES  
; APPLICANT: TREFFZER, AXEL  
; APPLICANT: BECHTHOLD, ANDREAS  
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
; FILE REFERENCE: 1974-005  
; CURRENT APPLICATION NUMBER: US/10/084,846A  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: DE 101 09 166.4  
; PRIOR FILING DATE: 2001-02-25  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; TYPE: PRT  
; LENGTH: 19608  
; ORGANISM: Streptomyces viridochromogenes  
; FEATURE:  
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.  
US-10-084-846A-8

Alignment Scores:  
Pred. No.: 0.0321 Length: 19608  
Score: 120.50 Matches: 49  
Percent Similarity: 35.71% Conservative: 16  
Best Local Similarity: 26.92% Mismatches: 92  
Query Match: 11.29% Indels: 25  
DB: 15 Gaps: 7

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)

QY 20 CCACGACACACAGAGCGCGGATCGGGCGGCAAGAGCTGTTTGTATGACC 79  
Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438

QY 80 TGGGGGGCGCAGAGCGATGAAGCTGGCGGTGTGACACCTTCTACGATAAGGTGCTGGCTG 139  
Db 5439 -----ProProAlaSerThrTrpArg-----SerThrAlaAlaCysTrpPro 5452  
QY 140 ACCGGAGCTGTGCGCTTCTTCGAGTCCCTGGAGCATGCAAGAGCAGAGATGAAGCAGG 199  
Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgProGlyArg 5470  
QY 200 TCAAGTTTCATGAGCTTCGTGTTTG---GGGGAGCAGACCAATACAAAGGCCGCAAGCATGT 256  
Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTrpCysProAlaCys 5490  
QY 257 ACGAGCGCACACCCCATCTGTTCAGGGCCAGCGGCTGGACCAACCGCCACTTTGACAAAGA 316  
Db 5491 ThrSerAsnArgProAlaArgProProThrSerSerTrpProThrArgProArgSerAla 5510  
QY 317 TCAACGAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376  
Db 5511 ProArgProSerThrSerArgSerThrAlaAlaGlyTrpProSerProAsnTrpSerArgAsp 5530  
QY 377 ACGCGCCGCGAGTGTGGAGTCCACCCGCGAGAAATTTGACTTNCCTCAACA-----ACT 430  
Db 5531 TrpProThrSerThrThrProSerProAlaArgThrArgThrAlaProSerArgArgThr 5550  
QY 431 GGCACCCCACTGATTTTCATTAAACCAACCCAGCCGCTGAGCGCTCATCCATCGATTTT 490  
Db 5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567  
QY 491 GAGCGGGAGCGCCAGTTTCCGAGCGCGCCAGGGGGCCAGGAGCGCTGCAATCGTTTG 550  
Db 5568 ArgProArgThrProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeu 5587  
QY 551 CCAGCC 556  
Db 5588 ProAla 5589

RESULT 8

US-10-437-963-166380  
; Sequence 166380, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 166380  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(276)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_65095C.1.pep  
US-10-437-963-166380

Alignment Scores:  
Pred. No.: 0.0149 Length: 276  
Score: 119.50 Matches: 52  
Percent Similarity: 35.08% Conservative: 15  
Best Local Similarity: 27.23% Mismatches: 69

```

Query Match: 11.20% Indels: 55
DB: 16 Gaps: 8
US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)

QY 29 CCACAGAGCGCGGAGCGGATCGCGCGCAAGAGCTGTTGATGACCTGGCGCGC 88
DB 3 ProArgArgArgArgArgileCysThrValArg----- 14
QY 89 CAGAGGCATGAAGCTGGCGGTGACACCTTCTACGATAAGTGCTGCGTACCGGAGC 148
DB 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25
QY 149 TGTGTCCTTCTCGAGTCCCTGGACATGCAAGACAGAGATGAAGCAGGTCAAGTTCA 208
DB 26 AlaSerProSerSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTGGCGGAGCAGCAATACAAAGGCGAGCATGTACGACG----- 262
DB 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACACGCCCATCTGTCAAGGCGCGCTCGACACCGCCACCTTGGACAGATCA 319
DB 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79
QY 320 ACAGTACCTTGGAGAGCGCTGC-----RAGAGATGGCGCTCAAGCAGGATGTA 370
DB 80 ArgSerGlySerCysArgGlyCysPheArgArgArgTrpArgSerThrArg----- 97
QY 371 TCAGCAGCGCCCGGAGTGGTGGAGTCCACCGCGAGCAATTTGACTTNCACCAACT 430
DB 98 -----ProAlaAlaProSerSerAlaSerProThrGly 108
QY 431 GGCACCCCACTGATTTCATTAAACCAACCCAGCCCTGAGGCTCATCTCCATGATTT 490
DB 109 AlaSerThrThrSer-----ProSerProThr----- 117
QY 491 GAGCGGGAGCGCCAGTTCGCCAGCGCGCCAGGGGGCCAGGAGCCTGCAAACTCGTTG 550
DB 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAspGlySer**Cys 133
QY 551 CGAGCCCTTGTGCATTGAAGCCATCAGCCA 583
DB 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

RESULT 9
US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI.pep
US-10-425-114-72136
Alignment Scores: 0.025 Length: 384
Pred. No.: 117 50 Matches: 69
Score:

```

```

Percent Similarity: 37.95% Conservative: 16
Best Local Similarity: 30.80% Mismatches: 74
Query Match: 11.01% Indels: 65
DB: 12 Gaps: 13
US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

QY 15 CGCGCCACACAGCAGC-----CACAGAGCGCGGAGCGGATGCGCGCGCAAGAGCT 68
DB 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln----- 69
QY 69 GTTTGATGACCTGGCGGCGCAGAGCATGAAGCTGGC----- 107
DB 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGTGCT 134
DB 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgAlaArgArgAspArgGlyAla 104
QY 135 GGCTGACCGCGGAGCTGCTCCCTCTTCGAGTCCCTGGACATGCA-----AGAGCA 185
DB 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaGlyArgAlaGluGlyArgGlyAla 124
QY 186 GAAGATGAAGCAGCTCAAGTTCATGAGCTTCGTTGGCGGAGCAGACCAATACAAGG 245
DB 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGCGACGCGCCATCTGTCAGGGCCA 287
DB 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CTGGACCAACCGCCACTTTGACCAAGATCAA 320
DB 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGACCGCTGCAAGAGATGGCGGT-----CAACGAGGATGT 368
DB 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGTGAGTCCACCGCGACGAAT---TTGACTTCCCAA 425
DB 202 Asp---ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuGlnGlyProA 221
QY 426 CAACTCGCACCAACTGATTTTCAATTAACCAACCCAGCCTGAGCGCTCATTCATCG 485
DB 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234
QY 486 ATTTTGAGCGGGAGCGCGCAGTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
DB 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGCCA 553
DB 253 roValPro 255

RESULT 10
US-10-425-114-72137
; Sequence 72137, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72137

```



LENGTH: 384  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3061-057-C6\_FLI.psp  
US-10-425-114-72137  
Alignment Scores:  
Pred. No.: 0.025 Length: 384  
Score: 117.50 Matches: 69  
Percent Similarity: 37.95% Conservativeness: 16  
Best Local Similarity: 30.80% Mismatches: 74  
Query Match: 11.01% Indels: 65  
DB: 12 Gaps: 13  
US-09-920-953-2 (1-598) x US-10-425-114-72137 (1-384)  
QY 15 CGCGGCCACAGC-----CACAGACGGCGGAGCGGATCGCGGCGCAGAGCT 69  
Db 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln----- 69  
QY 69 GTTTGATGACCTGCGCGCGCGAGCATGACATGCGC----- 107  
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgGlyGlu 84  
QY 108 ---GGTTGACACCTTCTACGA-----TAAGTGCT 134  
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspArgGlyAla 104  
QY 135 GGCTGACCGGAGCTGCTTTCGAGTCCTCGACATGCA-----AGAGCA 195  
Db 105 ArgAspGlyGlyAlaArgValLeuArgAlaGlyArgAlaGlyArgGlyAla 124  
QY 186 GAAGATGAGCAGCTCAAGTTTCATGCTTCGTTGGCGGAGCAGACCAATACAGGG 245  
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144  
QY 246 -----CGAGCATGTACGACGCACACGCCCTCTGCTCAGGCCCA 287  
Db 145 LeuGluGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164  
QY 288 CGG-----CCTGGACCCGCGCCTTTCACAGATCAA 320  
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183  
QY 321 GCAGTACTTGGAGACGCTGCGAGATGGGGT-----CAAGCAGATGT 368  
Db 184 AlaGlyValArgGlySer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201  
QY 369 GATCCAGCAGCGCGCGAGTGGTGGAGTCCACCGCGACGAAT---TTGACTTNCCTCA 425  
Db 202 Asp---ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221  
QY 426 CAATGCGCCCACTGATTTTCATTAAACCCACCGCCTGAGCGCTCATTCCTCG 485  
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234  
QY 486 ATTTGAGCGGGAGCGCCAGTTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545  
Db 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253  
QY 546 GTTTGCCA 553  
Db 253 roValPro 255  
RESULT 11  
US-10-084-846A-5  
Sequence 5, Application US/10084846A  
Publication No. US20040006026A1  
GENERAL INFORMATION:  
APPLICANT: WEITNAUER, GABRIELE  
APPLICANT: MUHLENWEG, AGNES  
APPLICANT: TREFFER, AXEL

APPLICANT: BECHTHOLD, ANDREAS  
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
FILE REFERENCE: 1974-005  
CURRENT APPLICATION NUMBER: US/10/084,846A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: PCT/EP01/09815  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: DE 101 09 166.4  
PRIOR FILING DATE: 2001-02-25  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 5  
LENGTH: 19723  
TYPE: PRT  
ORGANISM: Streptomyces viridochromogenes  
FEATURE:  
OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  
OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.  
US-10-084-846A-5  
Alignment Scores:  
Pred. No.: 0.0624 Length: 19723  
Score: 117.50 Matches: 64  
Percent Similarity: 32.91% Conservativeness: 13  
Best Local Similarity: 27.35% Mismatches: 86  
Query Match: 10.47% Indels: 71  
DB: 15 Gaps: 15  
US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)  
QY 556 GGCTGCGCAACGATTGAGGCTCTGGCGCCCTGGCGCGCTCGGC----- 509  
Db 16445 GlyAlaGlnArgArgCysHisArgThrGlyProGlyLysSerGlyAlaGlyProGly 16464  
QY 508 -----AACTGGCGCTCCCGCTCAAAATCATGGAATG 476  
Db 16465 ThrAlaAlaArgGlnArgLeuValArgSerArgTrpProMetSerAlaSerAlaPhe 16484  
QY 475 ACCGCTCAGCTGGGGTTGGTTAATGAAATCATGTTGGTGGCGAGTTGT----- 425  
Db 16485 SerTrpValGlyArgGly-----SerTrpAlaValSerCysAlaArgThr 16500  
QY 424 -----TGG-----GNAAGTCAAAATTCCT 407  
Db 16501 ProArgProGluProArgTrpArgArgSerProGlyGlyTrpArgTrpSerProCysArg 16520  
QY 406 CGCGCG-----TGGACTCCACCTCCGGCGGCTGTGATCATCATCTCTCTCTCA 356  
Db 16521 AlaGlySerSerTrpTrpSerPro---ProArgArgProGlyAsnTrpProThrSer 16539  
QY 355 CGCCCATCTCTGACAGCTCTCCCAAGTACTGCTTGTCTTGTCAAAGTGGCGTGT 296  
Db 16540 ThrProSer-----AlaArgThrArgTrpSerThrProSerAlaAlaThrGlyGlySer 16557  
QY 295 CCAGGCGCTGGCGCTTGACCATGGCGCTGTGCGT---CGTACATGCTTCGGCCCTTGT 239  
Db 16558 ProAsnGlyThrTrpArgProThrAlaArgCysArgProAlaAlaCysTrpThrArgCys 16577  
QY 238 ATTGCTGTCTCCGCCAAACAGAGCTCATGAATTCACCTGCTTCTCTCTCTCTT 179  
Db 16578 GlyGly-----ProArgAlaVal-----ProThrSerSerThrSerAla 16590  
QY 178 GCATGT-----CCAGGAGCTCGAAGAAGG--- 155  
Db 16591 GlnCysTrpSerThrAlaArgProArgProValaAsnArgProGlyProArgArgArgPro 16610  
QY 154 GCAGCAGCTCCGGGTCCAGCAGCCTTATCGTAGAAGGTGTCAACCCGCGCTTCATCC 95  
Db 16611 GlyArgArgProProThrAlaArgProAsnSerArgArgAlaArgPro-----Cys 16627  
QY 94 CTCTCTG-----CGCGCGCGCGGTCAACACAGCTTCTCTTGG----- 59  
Db 16628 TrpArgProProArgArgAlaSerTrpArgArgAlaCysCysGlySerProThrTrpPro 16647

QY 58 GCCCGCATCCCGCTTCCCGCTCTCTGTGGTGTCTGGTGGCG 17  
 Db 16648 GlyArgAlaProArgSerAlaCysSerAlaGlyTrpPro 16661

## RESULT 12

US-10-084-846A-7  
 ; Sequence 7, Application US/10084846A  
 ; Publication No. US20040006026A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEITNAUER, GABRIELE  
 ; APPLICANT: MUHLNBERG, AGNES  
 ; APPLICANT: TREPZER, AXEL  
 ; APPLICANT: BECHTHOLD, ANDREAS  
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
 ; FILE REFERENCE: 1974-005  
 ; CURRENT APPLICATION NUMBER: US/10/084,846A  
 ; CURRENT FILING DATE: 2003-02-25  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4  
 ; PRIOR FILING DATE: 2001-02-25  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 7  
 ; LENGTH: 19652  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces viridochromogenes  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.  
 ; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.  
 US-10-084-846A-7

Alignment Scores:  
 Pred. No.: 0.0777 Length: 19652  
 Score: 116.50 Matches: 73  
 Percent Similarity: 32.95% Conservative: 14  
 Best Local Similarity: 27.65% Mismatches: 93  
 Query Match: 10.38% Indels: 84  
 DB: 15 Gaps: 13

US-09-920-953-2 (1-598) x US-10-084-846A-7 (1-19652)

QY 598 GCGTGGTGGCAAAATGCTGATGCTCTTCAATGACG-----AAG 557  
 Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451  
 QY 556 GCGTGGCAAAATGCTGATGCTCTTCAATGACG-----AAG 557  
 Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451  
 QY 496 CCGCTCAAAATCGATGGAATGAGCTCAGGCTGGGGTGGTTAATCAAAATCAGTTGG 437  
 Db 6465 Prolie-----SerProThrArgAlaGlyProMet----- 6475  
 QY 436 GTGGCAGTTGTTGGNAAGTCAATTCGT----- 407  
 Db 6476 -----CysTrpSerSerTrpGlyArgProLysArgSerProThrProSerArgAla 6492  
 QY 406 CCGCGGTGGACT-----CCACCACCTCCGCGCGCTGGGATCA 368  
 Db 6493 ProGlyTrpThrArgThrAspValProArgProGlyArgSerThrArgSerGlyPro 6512  
 QY 367 CAGCTGTGACGCCCATCTCTTCAGCGCTCTCCAGGTACTGCTGTGATCTTGT--- 311  
 Db 6513 ArgProLeuThrSerArgSerLeuArgProAlaCysGlyThrAlaProHisThrVal 6532  
 QY 310 ---CAAAGTGGGGTGGTCCAGCGCGCTGGCTGGACAGATGGCGTGGCTGATCA 254  
 Db 6533 ArgArgSerSerHisGlyProThrThrGlyProProHisAlaGlyProArgArgMetPro 6552  
 QY 253 TGTCTGGCGCTTGTATGTTGTCTGCTCCGCCAACACGAACTCATGAATTTGACCT--- 197

Db 6553 AlaAlaLeuProGlySerGlyValIleuArgArgAlaAaGSerArgCysArgIleProArg 6572  
 QY 196 -----GCTTCATCTTCTGCTCTTGTGATGCTCCAGGACTCGAAGA--- 158  
 Db 6573 LeuArgArgProArgAlaArgSerArgProGlySerArgCysProCysProArgArgGlu 6592  
 QY 157 ---AGGCGACGAGCTCCGGTCCAGCCAGCA-----CCTTATCGTAGAAGGTGTCAACG 107  
 Db 6593 CysArgSerArgArgProArgArgProSerHisProAlaArgThrArgCysArgPro 6612  
 QY 106 CCAGCT-----TCATGC 95  
 Db 6613 ThrAlaArgProGlyThrTrpProAlaProArgValArgArgAlaGlyArgAla 6632  
 QY 94 CTTCTGCGCGCGCCAGGTCAACACAGCT----- 65  
 Db 6633 AlaAlaArgArgProHisArgSerAlaArgSerArgThrGlyCysArg 6652  
 QY 64 ---TCTTGGCGCGCATCCGCTCCGCGCTCTCTGT---GGTGTGGTGGCGCGCTCTG 11  
 Db 6653 ArgSer-ThrProAlaProArgArgAlaArgProAlaProGlyAlaGlyArgArgAl 6672  
 QY 10 CAGGCGAGCGC 1  
 Db 6672 aArgThrArg 6675

## RESULT 13

US-10-437-963-103601  
 ; Sequence 103601, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 103601  
 ; LENGTH: 155  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_101013C.1.pep  
 US-10-437-963-103601

Alignment Scores:  
 Pred. No.: 0.0315 Length: 155  
 Score: 115.50 Matches: 48  
 Percent Similarity: 36.91% Conservative: 7  
 Best Local Similarity: 32.21% Mismatches: 43  
 Query Match: 10.29% Indels: 45  
 DB: 16 Gaps: 9

US-09-920-953-2 (1-598) x US-10-437-963-103601 (1-155)

QY 385 CGCGCGCGCTGGATCATCATCTCTGTCACGCCATCTCTTCCAGCTCTCTCCAGGT 326  
 Db 19 ArgArgArgAlaProThrHisGluPro-----ProSerSerProArgAlaGlyArgSer 36  
 QY 325 ACTGCTTGATCTTGTCAAGTGGCGGT-----GGTCCAGCGCGTGGC 284  
 Db 37 ArgSerArgSerCysThrSerAlaProArgArgCysHisArgIleAlaProGlyArgGly 56  
 QY 283 -----CCTTACCCAGATGGCGCTGTCGCTGATACATGC 251



```
QY 54 CGGGCCAGAGAGCTGTTTGTGATGACCTGGGGGGGAGAGGCGATGAGCTGGCGGTGA 113
Db      |||
109 HisAlaaspArgGlyGlnHisValProGlyArgAlaArgGluArgArgGlyGln 128
QY 114 CACCTT-----CTAGATAAGGTGCTGCTCACCGGAGCTGCTGCCCTTCTTGA 164
Db      |||
129 HisCysHisAlaHisHisArgGluaspAlaalaTrpProGlyAlaArgValLeu----- 146
QY 165 GTCCCTGGACATGCA-----AGAGCA 185
Db      |||
147 GlyProGlyHisAlaGlyValProArgArgaspValAlaAlaValAlaArgVal 166
QY 186 GAAGATGAAGCAGGTCAAGTTCATGCTTCGTGTTGGCGGAGCAGACCAATACAGGG 245
Db      |||
167 HisLeuArgLeuProAlaValHisGlnArgArgValProHisArgGlnProaspGln--- 185
QY 246 CCGAAGCATGTACGAGC-----ACACGCCCATCTGCT--- 278
Db      |||
186 LeuArgHisValAlaaspProArgValGlyMetAlaProValAlaArgProArgGlyVal 205
QY 279 -----CAAGGCCACGGCTGGACCCGCCACTTTGACAAGATCAAGCAGTA 326
Db      |||
206 ProGlyArgArgHisGlyGlyArgGlyValHisProGlyHisAlaGlnGlnProGly 225
QY 327 CCTTGGAGAGACGCT-----GCAAGAGATGGCGCT 356
Db      |||
226 ProAlaArgGluAlaArgProArgProArgArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY 357 CAAGCAGGATGTATCCAGCAGCGCCGGAGTGTGGAGTCCACCCGCGACGAATTGA 416
Db      |||
246 Arg-----ArgArgArgArgValGlnArgHisProArgArgArgGly 259
QY 417 CTTNCCCAACACTGGCCACCACTGATTTTCATTACCCCAACCCAGCCTGAGCGCTC 476
Db      |||
260 AlaArgProGlnGluArgArgGlyArgValProAlaaspProAla-----AlaArg 276
QY 477 ATTCCATCGAATTTGAGCGGGAGCGCCAGTTGCCAGCGCGCCAGGGGCCCAGG 533
Db      |||
277 ValProAlaValProGlyHisGlyHisArgValProGlyValProGlnProHisArg 295
```

Search completed: July 19, 2004, 17:30:09  
Job time : 96 secs